



SEQUENCE LISTING

<110> NAKAJIMA, Hiroaki
NAGASAWA, Akitsu

<120> Method for giving resistance to weed control compounds to plants

<130> 0020-4764P

<140> 09/697,719

<141> 2000-10-27

<150> JP 10/120553

<151> 1998-04-30

<150> JP 10/281127

<151> 1998-10-02

<150> JP 10/330981

<151> 1998-11-20

<150> JP 11/054730

<151> 1999-03-02

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<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

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<210> 4

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ctt cgc ccc tcc ctc cat tcc cca acc tct ttc ttc acc tct ccc act	96
Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr	
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cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att	144
Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile	
35 40 45	
gcg gag gaa tcc acc gcg tct ccg ccc aaa acc aga gac tcc gcc ccc	192
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gtg gac tgc gtc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc	240
Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala	
65 70 75 80	
cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag	288
Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu	
85 90 95	
gcc cga gac cgc gtc ggc ggc aac atc acc acg atg gag agg gac gga	336
Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly	
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tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg	384
Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met	
115 120 125	
ctc acc atg gtg gtg gac agt ggt tta aag gat gag ctt gtt ttg ggg	432
Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly	
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gat cct gat gca cct cgg ttt gtg ttg tgg aac agg aag ttg agg ccg	480
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145 150 155 160	
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Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile	
165 170 175	
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Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	
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Lys	Ala	Ile	Gln	Glu	Arg	Asn	Gly	Ala	Ser	Lys	Pro	Pro	Arg	Asp	Pro	
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Leu	Thr	Met	Leu	Pro	Asp	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Asn	Lys	Val	
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Lys	Thr	Val	Val	Leu	Thr	Ile	Pro	Ser	Tyr	Val	Ala	Ser	Thr	Leu	Leu	
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Arg	Pro	Leu	Ser	Ala	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Lys	Phe	Tyr	Tyr	
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cct	cca	gtt	gct	gca	gtt	tcc	ata	tcc	tat	cca	aaa	gaa	gct	att	aga	1152
Pro	Pro	Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	
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Ser	Glu	Cys	Leu	Ile	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	
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Pro	Arg	Ser	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	
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cta	ttc	ccc	aac	cga	gca	cca	cct	gga	agg	gtt	cta	ctc	ttg	aat	tac	1296
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Ile	Gly	Gly	Ala	Thr	Asn	Thr	Gly	Ile	Leu	Ser	Lys	Thr	Asp	Ser	Glu	
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aat	gcc	cag	gat	cca	ttt	gta	gtg	ggg	gtg	aga	ctg	tgg	cct	caa	gct	1440
Asn	Ala	Gln	Asp	Pro	Phe	Val	Val	Gly	Val	Arg	Leu	Trp	Pro	Gln	Ala	
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Tyr	Val	Ser	Gly	Val	Ala	Leu	Gly	Arg	Cys	Val	Glu	Gly	Ala	Tyr	Glu	
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Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	
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Lys	Leu	Ser	Trp	Lys	Leu	Ser	Ser	Ile	Ser	Lys	Leu	Asp	Ser	Gly	Glu	

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Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu						
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Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr						
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Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg						
	370		375		380	
Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His						
385		390		395		400
Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser						
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Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr						
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Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu						
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Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala						
465		470		475		480
Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys						
	485		490		495	
Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn						
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Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu						
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<210> 10
<211> 34
<212> DNA
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<400> 14
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 <212> DNA
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<210> 16
 <211> 27
 <212> DNA
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<400> 16
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 Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro
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 65 70 75

aat gtg tat gac gtg atc gtg gtc ggt gga ggt ctc tcg ggc ctg gtg	286
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acg gag gct cgc gag cgc gtc ggc ggc aac att acg tcc atg tcg ggc	382
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Ser Met Leu Gln Ile Ala Val Asp Ser Gly Cys Glu Lys Asp Leu Val	
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Ile Pro Gly Lys Ile Arg Ala Gly Leu Gly Ala Ile Gly Leu Ile Asn	
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Gly Gln Leu His Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile
420 425 430
tac agc tcc agc ctg ttc ccc ggc cgc gcg ccc gag ggc cac atg ctg 1342
Tyr Ser Ser Ser Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu
435 440 445
ctg ctc aac tac atc ggc ggc acc acc aac cgc ggc atc gtc aac cag 1390
Leu Leu Asn Tyr Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln
450 455 460
acc acc gag cag ctg gtg gag cag gtg gac aag gac ctg cgc aac atg 1438
Thr Thr Glu Gln Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met
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Val Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val
480 485 490 495
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Trp Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu
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gac aag gcg cgc aag gcg ctg gac gcg gcg ggg ctg cag ggc gtg cac 1582
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515 520 525
ctg ggg ggc aac tac gtc agc ggt gtg gcc ctg ggc aag gtg gtg gag 1630
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530 535 540
cac ggc tac gag tcc gca gcc aac ctg gcc aag agc gtg tcc aag gcc 1678
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545 550 555
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Ala Val Lys Ala
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<210> 18

<211> 563

<212> PRT

<213> Chlamydomonas reinhardtii CC407

<400> 18

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35 40 45
Ala Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala
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Thr Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp
65 70 75
Asn Val Tyr Asp Val Ile Val Val Gly Gly Gly Leu Ser Gly Leu Val

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Arg	Pro	Val	Pro	Ser	Gly	Leu	Asp	Ala	Phe	Thr	Phe	Asp	Leu	Met	Ser
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			435					440					445		
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Trp	Pro	Arg	Ala	Ile	Pro	Gln	Phe	Asn	Leu	Gly	His	Leu	Glu	Gln	Leu
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<211> 32
<212> DNA
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<220>
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<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
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<400> 20
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<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 21
gctttagaat cggatcctat ggcagtggat gac 33

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 22
ggtgaacttc tatttgagct ctcaggtaaa tataag 36

<210> 23
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 23
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 <210> 24
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 <212> DNA
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 <220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 24
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 <210> 25
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 25
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 <210> 26
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 <212> DNA
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 <220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 26
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 <210> 27
 <211> 22
 <212> DNA
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 <220>
 <223> Designed oligonucleotides to synthesize genes encoding random peptides
 comprising 5 amino acids

 <220>
 <221> unsure
 <222> (1)...(22)
 <223> any n = a, g, c, t, any, unknown, or other

 <400> 27
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<210> 28
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<212> DNA
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<220>
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<222> (1)...(29)
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<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

<400> 29
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<210> 30
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 30
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<210> 31
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<400> 31
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<210> 32
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<212> DNA
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<220>
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<400> 32
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<210> 33
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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<400> 33
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<210> 34
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MGHASYS

<400> 34
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<210> 35
 <211> 26
 <212> DNA
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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<400> 35
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<210> 36
 <211> 26
 <212> DNA
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MGRASSL

<400> 36
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<210> 37
 <211> 23
 <212> DNA
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MGYAGY

<400> 37
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<210> 38
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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<400> 38
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<210> 39
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MGYAGF

<400> 39
 catgggttac gctggcttct aag 23

<210> 40
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MGYAGF

<400> 40
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<210> 41
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(HASYS)4

<400> 41
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<210> 42
 <211> 36

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(HASYS)4

 <400> 42
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 <210> 43
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(HASYS)4

 <400> 43
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 <210> 44
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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 <400> 44
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 <210> 45
 <211> 30
 <212> DNA
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 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(HASYS)8

 <400> 45
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 <210> 46
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 <400> 46
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<210> 47
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 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL) 4

 <400> 47
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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 <400> 48
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 <210> 49
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 <212> DNA
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 <400> 49
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 <212> DNA
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL) 4

 <400> 50
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 <210> 51
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 <212> DNA
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL) 8

<400> 51
 ctgcgtgctt cttccctgcg cgcattcttc 30

<210> 52
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL)8

<400> 52
 acgcagggaa gatgcgcgca gggaagaagc 30

<210> 53
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protoporphyrin IX binding protein HASYS

<400> 53
 His Ala Ser Tyr Ser
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<210> 54
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protoporphyrin IX binding protein MGHASYS

<400> 54
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<210> 55
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Protoporphyrin IX binding protein RASSL

<400> 55
 Arg Ala Ser Ser Leu
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<210> 56
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Protoporphyrin IX binding protein MGRASSL

<400> 56
Met Gly Arg Ala Ser Ser Leu
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<210> 57
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<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMpyP binding protein YAGY.

<400> 57
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<210> 58
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMpyP binding protein MGYAGY

<400> 58
Met Gly Tyr Ala Gly Tyr
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<210> 59
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> H2TMpyP binding protein YAGF

<400> 59
Tyr Ala Gly Phe
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<210> 60
<211> 6
<212> PRT
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<220>
<223> H2TMpyP binding protein MGYAGF

<400> 60
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<210> 61
<211> 22
<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(HASYS)4

<400> 61

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Ser His Ala Ser Tyr Ser
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<210> 62

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(HASYS)8

<400> 62

Met Gly His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr
1 5 10 15
Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser
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His Ala Ser Tyr Ser His Ala Ser Tyr Ser
35 40

<210> 63

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(RASSL)4

<400> 63

Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser
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Leu Arg Ala Ser Ser Leu
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<210> 64

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(RASSL)8.

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Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser
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Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu
20 25 30
Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu
35 40

<210> 65
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to introduce mutation into arabidopsis PPO gene

<400> 65
tggttcaggtg tttatgttgg tgatccttca aaactg 36

<210> 66
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify herbicide resistant arabidopsis PPO(A220V) gene

<400> 66
ccatgcggaa gcttatggag ttatctcttc tc 32

<210> 67
<211> 34
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify herbicide resistant arabidopsis PPO(A220V) gene

<400> 67
gggagattta atgtcgacca ttacttgta agcg 34

<210> 68
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify Arabidopsis chloroplast ferrochelatase gene

<400> 68
gatcggttct gaaatttgga tccatgcagg c 31

<210> 69
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Designed oligonucleotide primer to amplify Arabidopsis chloroplast ferrochelatase gene

<400> 69
 cacaaaacca acgagctcct ataggttccg g 31

<210> 70
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify soybean coproporphyrinogen III oxidase gene

<400> 70
 gaatcggatc cgaagcatga tgcattgtgc 30

<210> 71
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify soybean coproporphyrinogen III oxidase gene

<400> 71
 gggggtcgac tgatgaatta gatccattcc 30

<210> 72
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 72
 ggaagcttca agaatggcac aaattaacaa catggc 36

<210> 73
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 73
 gagtcgacgg tcatcaggca gccttcgtat cg 32

<210> 74
 <211> 1587
 <212> DNA

<213> Petunia hybrida EPSPS chloroplast transit peptide and Agrobacterium sp.
strain CP4 EPSPS

<220>

<221> CDS

<222> (1)...(1581)

<400> 74

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1 5 10 15	
aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt	96
Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu	
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gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt	144
Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val	
35 40 45	
ttg aaa aaa gat tca att ttt atg caa aag ttt tgt tcc ttt agg att	192
Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile	
50 55 60	
tca gca tca gtg gct aca gcc tgc atg ctt cac ggt gca agc agc cgg	240
Ser Ala Ser Val Ala Thr Ala Cys Met Leu His Gly Ala Ser Ser Arg	
65 70 75 80	
ccc gca acc gcc cgc aaa tcc tct ggc ctt tcc gga acc gtc cgc att	288
Pro Ala Thr Ala Arg Lys Ser Ser Gly Leu Ser Gly Thr Val Arg Ile	
85 90 95	
ccc ggc gac aag tgc atc tcc cac cgg tcc ttc atg ttc ggc ggt ctc	336
Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu	
100 105 110	
gcg agc ggt gaa acg cgc atc acc ggc ctt ctg gaa ggc gag gac gtc	384
Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val	
115 120 125	
atc aat acg ggc aag gcc atg cag gcc atg ggc gcc agg atc cgt aag	432
Ile Asn Thr Gly Lys Ala Met Gln Ala Met Gly Ala Arg Ile Arg Lys	
130 135 140	
gaa ggc gac acc tgg atc atc gat ggc gtc ggc aat ggc ggc ctc ctg	480
Glu Gly Asp Thr Trp Ile Ile Asp Gly Val Gly Asn Gly Gly Leu Leu	
145 150 155 160	
gcg cct gag gcg ccg ctc gat ttc ggc aat gcc gcc acg ggc tgc cgc	528
Ala Pro Glu Ala Pro Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg	
165 170 175	
ctg acc atg ggc ctc gtc ggg gtc tac gat ttc gac agc acc ttc atc	576
Leu Thr Met Gly Leu Val Gly Val Tyr Asp Phe Asp Ser Thr Phe Ile	
180 185 190	
ggc gac gcc tgc ctc aca aag cgc ccg atg ggc cgc gtg ttg aac ccg	624
Gly Asp Ala Ser Leu Thr Lys Arg Pro Met Gly Arg Val Leu Asn Pro	
195 200 205	
ctg cgc gaa atg ggc gtg cag gtg aaa tgc gaa gac ggt gac cgt ctt	672
Leu Arg Glu Met Gly Val Gln Val Lys Ser Glu Asp Gly Asp Arg Leu	
210 215 220	
ccc gtt acc ttg cgc ggg ccg aag acg ccg acg ccg atc acc tac cgc	720
Pro Val Thr Leu Arg Gly Pro Lys Thr Pro Thr Pro Ile Thr Tyr Arg	
225 230 235 240	
gtg ccg atg gcc tcc gca cag gtg aag tcc gcc gtg ctg ctc gcc ggc	768
Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly	
245 250 255	
ctc aac acg ccc ggc atc acg acg gtc atc gag ccg atc atg acg cgc	816

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 75
cacaggaaag gtaccatggt ctgcatcgcc cag 33

<210> 76
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

<400> 76
cctgcagctc gagagctcct actatttgta cac 33

<210> 77
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PPO variant in which a region presumed to be FAD binding site of PPO

<220>
<221> unknown
<222> (1)...(6)
<223> any Xaa = any amino acid, unknown, or other

<400> 77
Gly Xaa Gly Xaa Xaa Gly
1 5

<210> 78
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> PPO variant in which a region presumed to be FAD binding site of PPO

<400> 78
Gly Gly Gly Ile Ser Gly
1 5